to obtain phenograms according to the UPGMA method (SAHN-clustering) and by PCA (principal coordinate analysis).--

IN THE CLAIMS:

Please cancel claims 12-15 without prejudice or disclaimer of the subject matter contained therein.

Please amend the claims as follows:

1. (Amended) [Use of a primer or primer pair for DNA fingerprint analysis, characterized in that with the primer or primer pair a fingerprint is obtainable from humans as well as from animals as well as from plants as well as from microorganisms, and wherein the primer or primer pair hybridize to a DNA which codes the endonuclease, the reverse transcriptase or the RNAse H of a copia or copia-like element, in particular of coconut (Cocos nucifera L.).] A method for performing DNA-fingerprint analysis using a primer or primer pair comprising:

   (a) providing genomic DNA sequences from different species, wherein said DNA sequences encode an endonuclease, a reverse transcriptase or a RNAse H of a copia or copia-like element and wherein said DNA sequences are of animal, plant, human, prokaryotic or eukaryotic origin;

(b) subjecting said DNA sequences to a PCR reaction with a primer or primer pair, wherein said primer or primer pair hybridizes to said DNA sequences;

(c) separating the PCR products and;

(d) determining the degree of genetic relatedness between the DNA sequences.

2. (Amended) The [use] method according to claim 1, [characterized in that with the primer or primer pair a fingerprint is obtainable with] wherein the DNAs sequences [from the entire animal and plant kingdom, comprising] are derived from:

(a) the animal kingdom with all its subkingdoms, phylums, subphylums, families, genus and species[, preferably metazoa including the subphylums of the vertebrates, preferably the class of mammals, including in particular the family of the Hominids and the family of the Bovidae, including the species Bovis taurus and Ovis aries as well as all races and varieties which are derivable from the corresponding species];

(b) the plant kingdom with all its subkingdoms, phylums, subphylums, families, genus and species [, in particular Mycobionta and Cormobionta, preferably the division of the Spermatophyta, therein preferably the class of Monocotyledonae with its families of the Areaceae and its representatives of the species Cocos nucifera or the family of Poaceae with its representatives of the species Hordeum vulgare and Zea mays, in addition most preferably the class of the Dicotyledonae with its families, for example Solanaceae and its representatives of the species Solanum

tuberosum, Nicotiana tabacum, Petunia hybrida, or e.g., the family of Brassicaceae with its representative of the species Brassica napus or the family of the Chenopodiaceae with its representative Beta vulgaris or the family of Vitaceae with its representatives, for example, Vitis vinifera as well as all varieties and cultivars which are derivable from the corresponding species]; [and]

(c) humans; and

(d) microorganisms comprising prokaryotic microorganisms[, preferably gram-positive bacteria such as, for example, lactic acid bacteria, Sarcina and corynebacteria, and gram-negative bacteria such as, for example, Neisseria and enterobacteria,] and eukaryotic microorganisms [comprising fungi, preferably phycomycetes such as, for example, Phytophtora, and ascomycetes such as, for example, yeast].

3. (Amended) The [use according to claim 1 or 2]method according to claim 1, wherein[characterized in that] the DNAs to be analyzed [are amplified with the primer or primer pair via PCR and subsequently] are separated on a gel according to the length of the PCR products.

4. (Amended) The [use] method according to claim 3, [characterized in that] wherein the gel is a sequencing gel.

5. (Amended) The [use] method according to claim 3 or 4, [characterized in that in a further step a] further comprising the steps of performing a Southern blot and transferring the DNAs onto a membrane whereby hybridization can be visualized with a probe [Southern blot is performed and the DNAs transferred onto a membrane are visualized by hybridization with a probe].

6. (Amended) The [use] method according to claim 5, wherein [characterized in that] the probe is the primer or the primer pair hybridizes to said DNA sequences[of any one of the preceding claims].

7. (Amended) The [use] method according to claim 1[any one of claims 1 to 6], wherein[characterized in that] the primer or primer pair is labeled.

8. (Amended) The [use] method according to claim 7, [characterized in that] wherein the label is a non-radioactive label, [preferably digoxigenin,] biotin, a fluorescence dye, a dye or a radioactive label, [preferably ^{32}P].

9. (Amended) The [use] method according to any one of claims 1 to 8, wherein[characterized in that] the primer or primer pair [displays] corresponds to any one of the sequences [as represented in Table 2]selected from the group consisting of SEQ ID NOS 4-45.

10. (Amended) The [use] method according to claim 1[any one of claims 1 to 9], [characterized in that] wherein the primer or primer pair comprises a sequence which overlaps with any one of the sequences [represented in table 1 or 2]selected from the group consisting of SEQ ID NOS 4-45.

11. (Amended) The [use] method according to claim 1[any one of claims 1 to 10], [characterized in that] wherein the fingerprint analysis is used for studying biodiversity, genetic relationship, taxonomy[, and, in particular, in the field of forensic medicine, breeding, protection of plant varieties, gene library management, population genetics and for studies on evolution].

Please add the following new claims:

12. (New) The method according to claim 8, wherein the non-radioactive laebel is digoxigenin.

13. (New) The method according to claim 8, wherein the radioactive label is 75^{32} P.

14. (New) The method according to claim 2, wherein the DNAs sequences are derived from gram-positive or gram-negative bacteria.

15. (New) The method according to claim 2, wherein the DNAs sequences are derived from the class of Dicotyledonae.